

GenCore version 5.1.5
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Om protein - protein search, using sw model

Run on: August 1, 2003, 17:51:48 ; Search time 31 Seconds
(without alignments)
1154.677 Million cell updates/sec

Title: US-10-005-691-2
Perfect score: 4351
Sequence: 1 MLFTVSCSKMSSTIVDRDDSS...QQQLSRHRTDSLPPDSKVQPO 846
Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5
Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	4351	100.0	846	3 US-08-885-291-55
2	4351	100.0	846	3 US-09-107-847-2
3	4351	100.0	846	3 US-09-496-672-55
4	4149.5	95.4	855	2 US-08-816-693A-2
5	4149.5	95.4	855	3 US-08-885-291-2
6	4149.5	95.4	855	3 US-09-496-672-2
7	4149.5	95.4	855	4 US-09-618-425-11
8	1966.5	45.2	824	2 US-08-785-310A-7
9	1960.5	45.1	824	3 US-08-885-291-52
10	1960.5	45.1	824	3 US-09-496-672-52
11	1957.5	45.0	824	2 US-08-816-693A-52
12	1948	44.8	816	2 US-08-785-310A-8
13	1941	44.6	816	2 US-08-816-693A-53
14	1941	44.6	816	3 US-08-885-291-53
15	1941	44.6	816	3 US-09-496-672-53
16	1916.5	44.0	747	2 US-08-816-693A-51
17	1916.5	44.0	747	3 US-08-885-291-51
18	1916.5	44.0	747	3 US-09-496-672-51
19	457	10.5	626	4 US-08-971-188-10
20	457	10.5	626	4 US-09-374-454-21
21	437.5	10.1	625	4 US-09-618-425-13
22	430	9.9	789	4 US-08-971-188-9
23	430	9.9	789	4 US-09-374-454-22
24	424.5	9.8	602	4 US-09-374-454-19
25	412.5	9.5	1507	4 US-09-914-259-37
26	405.5	9.3	870	1 US-08-785-241-4
27	405.5	9.3	870	4 US-09-374-454-6

ALIGNMENTS

RESULT 1
US-08-885-291-55
; Sequence 55, Application US/08885291A
; Patent No. 6057125
; GENERAL INFORMATION:
; APPLICANT: Takahashi, Joseph S.
; APPLICANT: Turek, Fred W.
; APPLICANT: Pinto, Lawrence H.
; TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
; FILE REFERENCE: 0290-5
; CURRENT APPLICATION NUMBER: US/08/885,291A [6057125]
; EARLIER FILING DATE: 1997-06-30
; EARLIER APPLICATION NUMBER: 08/816,693 / 9613
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 55
; LENGTH: 846
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-885-291-55

Query Match Best Local Similarity 100.0%; Score 4351; DB 3; Length 846;
Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLFTVSCSKMSSTIVDRDDSSIFDGIVEDDKAKRVRNSRNKEKKRDOFNVLIKELGSM 60
Db 1 MLFTVSCSKMSSTIVDRDDSSIFDGIVEDDKAKRVRNSRNKEKKRDOFNVLIKELGSM 60

QY 61 LPGNARKMDKSTVLOQSKDIFLRLKHKETITAQSDASEIRODWKPTTLSNEEFOLMLEALDG 120
Db 61 LPGNARKMDKSTVLOQSKDIFLRLKHKETITAQSDASEIRODWKPTTLSNEEFOLMLEALDG 120

QY 121 FFLAIMTDGSIIYVSESVTSLLEHPLSDLVQDOSIFNFTPEGESEVYLSTHLESDSL 180
Db 121 FFLAIMTDGSIIYVSESVTSLLEHPLSDLVQDOSIFNFTPEGESEVYLSTHLESDSL 180

QY 181 TPPEYLKSKNOLEFFCCHMLRGITDPKEPSTYEVKFIGNFKSINSVSSAHDNGFEGTIQT 240
Db 181 TPPEYLKSKNOLEFFCCHMLRGITDPKEPSTYEVKFIGNFKSINSVSSAHDNGFEGTIQT 240

QY 241 HRPSYEDRVCFVATVRLATPQFIKEMCTVEEPNEEHTSRHSLENKFLFIDHRAPPINGYL 300
Db 241 HRPSYEDRVCFVATVRLATPQFIKEMCTVEEPNEEHTSRHSLENKFLFIDHRAPPINGYL 300

QY 301 PFEVLGTSQYDYYHVDLLENLAKCHEHLMQYKGKSCCYRFLKGQWIMQTHYYITYH 360
Db 301 PFEVLGTSQYDYYHVDLLENLAKCHEHLMQYKGKSCCYRFLKGQWIMQTHYYITYH 360

QY 361 QWNSRPEFIVCHTVVSYAERERRELGIEESIPEATAADKSQDSGDSDNRINTVSKA 420
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 Db 351 QWNSRPEFIVCHTVVSYAERERRELGIEESIPEATAADKSQDSGDSDNRINTVSKA 420
 QY 421 LERFDHSPTPSASSRRSSRKSSHTAVSDPSSTPTKIPDTSTPPRQLPAHEKMVQRSSF 480
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 421 LERFDHSPTPSASSRRSSRKSSHTAVSDPSSTPTKIPDTSTPPRQLPAHEKMVQRSSF 480
 QY 481 SSQSINSQSOSVGSSLTOPVMSQATNLPIPOGMSOFOFSAQIGAMQHLKDQEORTMIEAN 540
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 Db 481 SSQSINSQSOSVGSSLTOPVMSQATNLPIPOGMSOFOFSAQIGAMQHLKDQEORTMIEAN 540
 QY 541 THROQEELRKIQEQLQMVGQGLQMFLQSNPGQINFGSVQLSSGNSSNIQOLAPINMQQ 600
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 Db 541 IHRQEEELRKIQEQLQMVGQGLQMFLQSNPGQINFGSVQLSSGNSSNIQOLAPINMQQ 600
 QY 601 VVPTNQI0SGMNTGHIGTTQHMIQQTLOSTSTQSQNVLSGHSQQTSLPSQTOSTLTA 660
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 Db 601 VVPTNQI0SGMNTGHIGTTQHMIQQTLOSTSTQSQNVLSGHSQQTSLPSQTOSTLTA 660
 QY 661 LYNTMVISOPAGSMVQIPSSMPNSTQSAAVTFTQDROIRFSOGQQLVTKLVTA 720
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 Db 661 LYNTMVISOPAGSMVQIPSSMPNSTQSAAVTFTQDROIRFSOGQQLVTKLVTA 720
 QY 721 GAVMVPSSTMGMQWVTAYPEFAEQQCSQTLTSVHQOQQQSSQEQQLTSVQPSQAQLTQ 780
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 Db 721 GAVMVPSSTMGMQWVTAYPEFAEQQCSQTLTSVHQOQQQSSQEQQLTSVQPSQAQLTQ 780
 QY 781 PPOQFLQTSRLHGNPSTQOLISAAFPLOQSTTPQSHHQHQHSQQQQQLSRHRTDSLDP 840
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 Db 781 PPOQFLQTSRLHGNPSTQOLISAAFPLOQSTTPQSHHQHQHSQQQQQLSRHRTDSLDP 840
 QY 841 SKVQPO 846
 ||||||| |||||||
 Db 841 SKVQPO 846

RESULT 2
 US-09-107-847-2
 Sequence 2, Application US/09107847
 Patent No. 610062
 GENERAL INFORMATION:
 APPLICANT: DUCKWORTH, DAVID
 TITLE OF INVENTION: NOVEL USE
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ratner & Prestia
 STREET: P.O. Box 980
 CITY: Valley Forge
 STATE: PA
 COUNTRY: USA
 ZIP: 19482
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,847
 FILING DATE: 30-JUN-1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 97304996.8
 FILING DATE: 08-JUL-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Prestia, Paul F
 REGISTRATION NUMBER: 23, 031
 REFERENCE/DOCKET NUMBER: GH-30003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEX:

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 846 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

Us-09-107-847-2

Query Match 100.0%; Score 4351; DB 3; Length 846;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Query 1 MLFTVSCSKMSIVDRDDSIFDGIVEDDKAKRVRSRNKSERRDQFVNLIKELGM 60
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 Db 1 MLFTVSCSKMSIVDRDDSIFDGIVEDDKAKRVRSRNKSERRDQFVNLIKELGM 60
 QY 61 LPGNARKMDKSTVLOKSIDFLRKHEITAQDASERDWDKPTTLSNEERTQMLALDG 120
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 Db 61 LPGNARKMDKSTVLOKSIDFLRKHEITAQDASEIRQDWKPTTLSNEERTQMLALDG 120
 QY 121 FFLAINTMDGSIIVYSESVTSLIEHLPSDLWDQSFNTPEGEHSEYVKTISTHLES 180
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 121 FFLAINTMDGSIIVYSESVTSLIEHLPSDLWDQSFNTPEGEHSEYVKTISTHLES 180
 QY 181 TPEYLSKSNQLEFCCHMLRGTIDPKEPSTYEVKFIGNETSFHRSLEWKFLFDHRAPPIGYL 300
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 181 TPEYLSKSNQLEFCCHMLRGTIDPKEPSTYEVKFIGNETSFHRSLEWKFLFDHRAPPIGYL 300
 QY 241 HRPSEYDRVCVFATVRLATPQFIKEMCTVEEPNEEFTSRSLIENKFLLDHRAPPIGYL 300
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 Db 241 HRPSEYDRVCVFATVRLATPQFIKEMCTVEEPNEEFTSRSLIENKFLLDHRAPPIGYL 300
 QY 301 PFEVLTGTYDYYHDDLENLAKCHEHLMQYKGKGSCTYRELTKGQOWTWLQTHYT 360
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 Db 301 PFEVLTGTYDYYHDDLENLAKCHEHLMQYKGKGSCTYRELTKGQOWTWLQTHYT 360
 QY 361 QWNSRPEFIVCHTVVSYAERERRELGIEESIPEATAADKSQDSGDSDNRINTVSKA 420
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 Db 361 QWNSRPEFIVCHTVVSYAERERRELGIEESIPEATAADKSQDSGDSDNRINTVSKA 420
 QY 421 LERFDHSPTPSASSRRSSRKSSHTAVSDPSSTPTKIPDTSTPPRQLPAHEKMVQRSSF 480
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 Db 421 LERFDHSPTPSASSRRSSRKSSHTAVSDPSSTPTKIPDTSTPPRQLPAHEKMVQRSSF 480
 QY 481 SSQSINSQSOSVGSSLTOPVMSQATNLPIPOGMSOFOFSAQIGAMQHLKDQEORTMIEAN 540
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 Db 481 SSQSINSQSOSVGSSLTOPVMSQATNLPIPOGMSOFOFSAQIGAMQHLKDQEORTMIEAN 540
 QY 541 IHRQEEELRKIQEQLQMVGQGLQMFLQSNPGQINFGSVQLSSGNSSNIQOLAPINMQQ 600
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 Db 541 IHRQEEELRKIQEQLQMVGQGLQMFLQSNPGQINFGSVQLSSGNSSNIQOLAPINMQQ 600
 QY 601 VVPTNQI0SGMNTGHIGTTQHMIQQTLOSTSTQSQNVLSGHSQQTSLPSQTOSTLTA 660
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 Db 601 VVPTNQI0SGMNTGHIGTTQHMIQQTLOSTSTQSQNVLSGHSQQTSLPSQTOSTLTA 660
 QY 661 LYNTMVISOPAGSMVQIPSSMPNSTQSAAVTFTQDROIRFSOGQQLVTKLVTA 720
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 Db 661 LYNTMVISOPAGSMVQIPSSMPNSTQSAAVTFTQDROIRFSOGQQLVTKLVTA 720
 QY 721 GAVMVPSSTMGMQWVTAYPEFAEQQCSQTLTSVHQOQQQSSQEQQLTSVQPSQAQLTQ 780
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 Db 721 GAVMVPSSTMGMQWVTAYPEFAEQQCSQTLTSVHQOQQQSSQEQQLTSVQPSQAQLTQ 780
 QY 781 PPOQFLQTSRLHGNPSTQOLISAAFPLOQSTTPQSHHQHQHSQQQQQLSRHRTDSLDP 840
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 Db 781 PPOQFLQTSRLHGNPSTQOLISAAFPLOQSTTPQSHHQHQHSQQQQQLSRHRTDSLDP 840
 QY 841 SKVQPO 846
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 Db 841 SKVQPO 846